

Mon Sep 8 07:48:44 2003

us-10-08

FT DOMAIN 101 195 PLASTOCYANIN-LIKE 1.  
FT DOMAIN 245 346 PLASTOCYANIN-LIKE 2.  
FT DOMAIN 368 387 4 X 5 AA TANDEM REPEATS OF A-A-S-A-P.  
FT REPEAT 368 372 1.  
FT REPEAT 373 377 2.  
FT REPEAT 378 382 3.  
FT REPEAT 383 387 4.  
SQ SEQUENCE 392 AA; 40954 MW; A4707CC87B923C97 CRC64;

Query Match 52.8%; Score 1386; DB 1; Length 392;  
Best Local Similarity 69.5%; Pred. No. 4.4e-90;  
Matches 264; Conservative 44; Mismatches 66; Indels 6; Gaps 3;

QY 11 LICALSALMLSGCSNQADKAAQPKSSTVDAAKTA-NADNAASQEHQGLPVIDAIVTHA 69  
Db 9 MIASLPALACG---GEQAAQAPAEPPAASAAASAAQATAETPAGELPVIDAVTTHA 64  
QY 70 PEVPPPVDHRDHPAKVVKMETVEKVMRLADGVEYQFWTFGGQVPGQMIRVREGDTIEVQF 129  
Db 65 PEVPPAIDRDYPKVRVKMETVEKTMKMDGVEYRYWTFDGDVPGRMIRVREGDTVEVEF 124  
QY 130 SNHPDSKMPHNVDFAATGPGGGAEASFTAPGHTSTFSFKALQPGLYVYHCAVAPVGMHI. 189  
Db 125 SNNPSTVPHNVDFHAATGQGGGAAATFTAPGRTSTFSFKALQPGLYIYHCAVAPVGMHI 184  
QY 190 ANGMYGLILVEPKGLPKVDKEYVVMQGDFTYTKGKYGEQGLQPFDMKAIREDAEYVVFN 249  
Db 185 ANGMYGLILVEPKGLPKVDKEYVIVQGDFTYTKGKGAQGLQPFDMKAVAEQPEYVVFN 244  
QY 250 GSVGALTGENALKAKVGETVRLFVNGGPNLTSSPHVIGEIPDKVHFEGGKGENHNIQTT 309  
Db 245 GHVGSAGDNALKAKAGETVRMYVNGGPNLVSSPHVIGEIPDKVYVEGGKLINENVQST 304  
QY 310 LIPAGGAAITEFKVDVPGDYVLVDHAIFFRAFNGKALGILKVEGEENHEIYSHKQTDVAVYL 369  
Db 305 IVPAGGSAIVEFKVDIPGSYTLVDHSIFRAFNGKALGQLKVEGAENPEIMTQKLSDTAYA 364  
QY 370 PEGAPQAIDTQEAAPKTPAPA 389  
Db 365 GSGAASA-PAASAPAASAPA 383

RESULT 2

NIR\_RHOSH

ID NIR\_RHOSH STANDARD; PRT; 374 AA.  
AC Q53239;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Copper-containing nitrite reductase precursor (EC 1.7.2.1) (Cu-NIR).  
GN NIRK.  
OS Rhodobacter sphaeroides (Rhodopseudomonas sphaeroides).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales;  
OC Rhodobacteraceae; Rhodobacter.  
OX NCBI\_TaxID=1063;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2.4.3;  
RX MEDLINE=97175533; PubMed=9023188;  
RA Tosques I.E., Kwiatkowski A.V., Shi J., Shapleigh J.P.;  
RT "Characterization and regulation of the gene encoding nitrite  
reductase in Rhodobacter sphaeroides 2.4.3.";  
RL J. Bacteriol. 179:1090-1095 (1997).  
CC -1- CATALYTIC ACTIVITY: Nitric oxide + H(2)O + ferricytochrome c =  
nitrite + ferrocycytochrome c.  
CC -1- COFACTOR: CONTAINS ONE ATOM OF TYPE I COPPER AND ONE ATOM OF TYPE  
II COPPER; FAD. TYPE I COPPER IS BOUND WITHIN A SINGLE MONOMER,  
WHILE TYPE 2 COPPER IS HELD BY RESIDUES FROM EACH OF TWO MONOMERS  
OF THE TRIMER. NITRITE IS BOUND TO THE TYPE 2 COPPER SITE.  
CC PSEUDOAZURIN IS THE PHYSIOLOGICAL ELECTRON DONOR FOR THE CU-NIR IN  
VITRO (BY SIMILARITY).  
CC -1- PATHWAY: Nitrate assimilation (denitrification).  
CC SUBUNIT: Homotrimer (By similarity).

Doc in 179 -  
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|    |       |     |      |   |            |        |             |
|----|-------|-----|------|---|------------|--------|-------------|
| 34 | 109   | 4.2 | 108  | 1 | C555_CHLTE | Q8kg93 | chlorobium  |
| 35 | 109   | 4.2 | 1062 | 1 | CERU_MOUSE | Q61147 | mus musculu |
| 36 | 108   | 4.1 | 527  | 1 | LAC5_TRAVE | Q12717 | trametes ve |
| 37 | 107.5 | 4.1 | 520  | 1 | LAC2_AGABI | Q12542 | agaricus bi |
| 38 | 107.5 | 4.1 | 1257 | 1 | CCAA_BACTU | Q45754 | bacillus th |
| 39 | 107.5 | 4.1 | 2647 | 1 | FLNA_HUMAN | P21333 | homo sapien |
| 40 | 107   | 4.1 | 1654 | 1 | OMPB_RICRI | Q53047 | r outer mem |
| 41 | 106.5 | 4.1 | 485  | 1 | IMDH_PYRAB | Q9uy49 | pyrococcus  |
| 42 | 106.5 | 4.1 | 599  | 1 | LAC2_THACU | Q02075 | thanatephor |
| 43 | 106.5 | 4.1 | 642  | 1 | PHSA_STRAT | Q53692 | streptomyce |
| 44 | 105.5 | 4.0 | 739  | 1 | PURL_CAUCR | Q9a5f0 | caulobacter |
| 45 | 105   | 4.0 | 86   | 1 | C555_CHLLT | P00123 | chlorobium  |

## ALIGNMENTS

## RESULT 1

ANIA\_NEIGO

ID ANIA\_NEIGO STANDARD; PRT; 392 AA.

AC Q02219;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Major outer membrane protein Pan 1 precursor.

GN ANIA.

OS Neisseria gonorrhoeae.

OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;

OC Neisseriaceae; Neisseria.

OX NCBI\_TaxID=485;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R10;

RX MEDLINE=93014187; PubMed=1383156;

RA Hoehn G.T., Clark V.L.;

RT "Isolation and nucleotide sequence of the gene (aniA) encoding the

RT major anaerobically induced outer membrane protein of Neisseria

RT gonorrhoeae.";

RL Infect. Immun. 60:4695-4703(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 33084 / F62;

RX MEDLINE=93014188; PubMed=1398981;

RA Hoehn G.T., Clark V.L.;

RT "The major anaerobically induced outer membrane protein of Neisseria

RT gonorrhoeae, Pan 1, is a lipoprotein.";

RL Infect. Immun. 60:4704-4708(1992).

CC -!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid

CC anchor. (Probable).

CC -!- INDUCTION: BY ANAEROBIOSIS.

CC -!- SIMILARITY: Contains 2 plastocyanin-like domains.

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DR EMBL; M97926; AAA25462.1; -.

DR PIR; A49208; A49208.

DR PDB; 1KBV; 27-FEB-02.

DR PDB; 1KBW; 27-FEB-02.

DR InterPro; IPR001117; Cu-oxidase.

DR InterPro; IPR001287; CuNO2 reductase.

DR Pfam; PF00394; Cu-oxidase; 2.

DR PRINTS; PR00695; CUNO2RDTASE.

DR PROSITE; PS00013; PROKAR LIPOPROTEIN; 1.

KW Repeat; Outer membrane; Lipoprotein; Signal; 3D-structure.

FT SIGNAL 1 18

FT CHAIN 19 392 MAJOR OUTER MEMBRANE PROTEIN PAN 1.

FT LIPID 19 19 N-ACYL DIGLYCERIDE (PROBABLE).

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